

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 20, 1999, 15:16:41 ; Search time 10.22 seconds

(without alignments)
926,603 million cell updates/sec

Title: US-09-126-945-2

Perfect score: 1795
Sequence: 1 MGSASPCISVSPSHLLP.....GTRRDISORLYGVHP3135

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

Database: SwissProt_37.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	354	19.8	114	ETS4_DROME	P29775 drosophila
2	300.5	16.8	462	ERG_HUMAN	P11308 homo sapien
3	294	16.5	464	ELK_MOUSE	Q04688 drosophila
4	282	15.4	458	ETS4_DROME	Q04687 gallus galli
5	282	15.4	458	ETS4_DROME	Q04687 gallus galli
6	288	16.1	669	MYB_AVILE	P01105 avian leuko
7	277	15.5	454	GABR_MOUSE	Q00422 mus musculu
8	275	15.4	453	FLU1_XENLA	P11357 xenopus lae
9	272	15.2	485	ETS4_DROME	P15062 gallus galli
10	270	15.1	452	FLU1_MOUSE	P16323 mus musculu
11	265.5	14.9	485	ETS4_DROME	Q04687 gallus galli
12	265.5	14.9	485	ETS4_DROME	Q04687 gallus galli
13	252.5	14.5	441	ETS4_DROME	P11357 xenopus lae
14	250	14.0	472	ETS4_DROME	P11357 xenopus lae
15	247.5	13.9	829	ETS4_DROME	P11357 xenopus lae
16	247.5	13.9	829	ETS4_DROME	P11357 xenopus lae
17	247.5	13.9	829	ETS4_DROME	P11357 xenopus lae
18	246.5	13.8	469	ETS4_DROME	P11357 xenopus lae
19	246	13.8	468	ETS4_DROME	P11357 xenopus lae
20	244.5	13.7	438	ETS4_DROME	P11357 xenopus lae
21	243.5	13.6	440	ETS4_DROME	P11357 xenopus lae
22	243.5	13.6	440	ETS4_DROME	P11357 xenopus lae
23	243.5	13.6	440	ETS4_DROME	P11357 xenopus lae
24	240.5	13.5	441	ETS4_DROME	P11357 xenopus lae
25	237	13.3	479	ETS4_DROME	P11357 xenopus lae
26	236	13.2	510	ERM_HUMAN	P11357 xenopus lae
27	233.5	13.1	612	ELF1_HUMAN	Q06075 mus musculu
28	233.5	13.1	612	ELF1_HUMAN	Q06075 mus musculu
29	224	12.5	428	ELF1_HUMAN	Q06075 mus musculu
30	224	12.5	429	ELF1_HUMAN	Q06075 mus musculu
31	224	12.5	429	ELF1_HUMAN	Q06075 mus musculu
32	222	12.3	553	ETS4_DROME	P11357 xenopus lae
33	222	12.3	553	ETS4_DROME	P11357 xenopus lae
34	217.5	12.2	477	ETS4_DROME	P11357 xenopus lae
35	216.5	12.1	431	SAPB_HUMAN	P28323 homo sapien
36	216.5	12.1	431	SAPB_HUMAN	P28323 homo sapien
37	212.5	11.9	477	ETS4_DROME	P11357 xenopus lae
38	210.5	11.8	430	SAPB_MOUSE	P11357 xenopus lae
39	208.5	11.7	523	ETS4_DROME	P11357 xenopus lae
40	208.5	11.7	523	ETS4_DROME	P11357 xenopus lae
41	203.5	11.3	941	ETS4_DROME	P11357 xenopus lae
42	203.5	11.3	941	ETS4_DROME	P11357 xenopus lae
43	199	11.1	250	ETS4_DROME	P11357 xenopus lae

ALIGNMENTS

Result ID	Score	Query Match	Length	DB ID	Description
1	354	19.8	114	ETS4_DROME	P29775 drosophila
2	300.5	16.8	462	ERG_HUMAN	P11308 homo sapien
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4	282	15.4	458	ETS4_DROME	Q04687 gallus galli
5	282	15.4	458	ETS4_DROME	Q04687 gallus galli
6	288	16.1	669	MYB_AVILE	P01105 avian leuko
7	277	15.5	454	GABR_MOUSE	Q00422 mus musculu
8	275	15.4	453	FLU1_XENLA	P11357 xenopus lae
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17	247.5	13.9	829	ETS4_DROME	P11357 xenopus lae
18	246.5	13.8	469	ETS4_DROME	P11357 xenopus lae
19	246	13.8	468	ETS4_DROME	P11357 xenopus lae
20	244.5	13.7	438	ETS4_DROME	P11357 xenopus lae
21	243.5	13.6	440	ETS4_DROME	P11357 xenopus lae
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23	243.5	13.6	440	ETS4_DROME	P11357 xenopus lae
24	240.5	13.5	441	ETS4_DROME	P11357 xenopus lae
25	237	13.3	479	ETS4_DROME	P11357 xenopus lae
26	236	13.2	510	ERM_HUMAN	P11357 xenopus lae
27	233.5	13.1	612	ELF1_HUMAN	Q06075 mus musculu
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33	222	12.3	553	ETS4_DROME	P11357 xenopus lae
34	217.5	12.2	477	ETS4_DROME	P11357 xenopus lae
35	216.5	12.1	431	SAPB_HUMAN	P28323 homo sapien
36	216.5	12.1	431	SAPB_HUMAN	P28323 homo sapien
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38	210.5	11.8	430	SAPB_MOUSE	P11357 xenopus lae
39	208.5	11.7	523	ETS4_DROME	P11357 xenopus lae
40	208.5	11.7	523	ETS4_DROME	P11357 xenopus lae
41	203.5	11.3	941	ETS4_DROME	P11357 xenopus lae
42	203.5	11.3	941	ETS4_DROME	P11357 xenopus lae
43	199	11.1	250	ETS4_DROME	P11357 xenopus lae

```

Query Match      16.8%  Score 300.5;  DB 1;  Length 462;
Best Local Similarity 26.7%  Pred. No. 3.7e-16;
Matches 103;  Conservative 48;  Mismatches 118;  Indels 117;  Gaps 17;

0Y  45 PAPPAPPGGASNF-----YLSYEDL-----YPEDSSMAKAPASSSE 84
      | | | | |
      4

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EMBL; X68259; G7943; -

Query Match 15.4%; Score 275; DB 1; Length 453;
 Best Local Similarity 32.4%; Pseq. No. 3.4e-14;
 Matches 78; Conservative 29; Mismatches 78; Indels 56; Gaps 9;

143 LTPADPMKSSNNYKMLTETHTYRPMVC-VAQELACKELCMSEEP-ROSPPLGSD 200
 125 VADPALMSODHYRMLBMAKKEIGVIGLCSQVNDLCKSKSKEDLSTSYTNE 184
 201 VLAHMDIKMSAA-----FMKETSPP----- 222
 185 VLLSHLNTLRDSSSLQVNTQMTDQSSRLTAKEDPEYEAVRSGMGKMSNPVTKSPM 244
 222 GAHTCASTEESN-----TDEYDSSCSQPIHLMQFLKELLKPHSYGRFIR 270
 245 GGTQVNNKSDQQRSQDPDYOILGTFSSRLAMPSSQ-IGMOPFLLE-LTSSSSNACT 302
 271 WLKKEGFIKEDSNQVATLWGIKRRKPAANTDKLSRQYKCIIRPDISQILYQ 330
 303 W-EGTNGEFMTDPEVARHWCERKSKNPKNMDLSTALRYTYSIMTKVH-CKRYAVK 360
 331 F 331
 361 F 361

RESULT 9
 ETSB CHICK STANDARD; PRT; 485 AA.
 AD P18663
 DT 01-AUG-1990 (REL. 15. CREATED)
 DT 01-AUG-1990 (REL. 15. LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31. LAST ANNOTATION UPDATE)
 DE TRANSFORMING PROTEIN P68/C-ETS-1.
 GN ETS-1.
 OS GALLUS GALLUS (CHICKEN).
 NC NUKARLOVA, METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
 CC GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
 RN [1] UNKNTIMBL; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
 RP SEQUENCE FROM N.A.
 RA LEPRINCE D., DUTERQUE-COUILAUD M., LI R.-P., HENRY C., FLOURENS A.,
 DEBURE B., STEHELIN D.;
 RA Alternative splicing within the chicken ets-1 locus: implications
 for proto-oncogene.
 RT J. VIROL. 63:3233-3241(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 88206088.
 RA MEDLSON D.R., MCWILLIAMS W.J., PAPAS T.S.;
 RT Molecular cloning and isolation of the chicken ets locus.*
 RT VIROLOGY 164:98-103(1988).
 CC -1- FUNCTION: THIS PROTEIN IS THE NORMAL CELLULAR PRODUCT OF CHICKEN
 ETS. IN THE E26 VIRUS, ETS IS RESPONSIBLE FOR ANTIBLAST
 TRANSFORMATION.
 CC -1- TISSUE SPECIFICITY: SPLEEN.
 CC -1- ALTERNATIVE PRODUCTS: ALTERNATIVE SPLICING MECHANISM WITHIN THE
 EXTREME 5' AND 3' UNTRANSLATED REGIONS OF THE ETS-1 GENE.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.

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 CC EMBL: M21833; G211464; -;
 DR EMBL: M20515; G211464; ALT INIT.
 DR EMBL: M20507; G211464; JOINED.

DR EMBL: M20508; G211464; JOINED.
 DR EMBL: M20509; G211464; JOINED.
 DR EMBL: M20510; G211464; JOINED.
 DR EMBL: M20511; G211464; JOINED.
 DR EMBL: M20512; G211464; JOINED.
 DR EMBL: M20513; G211464; JOINED.
 DR EMBL: M20514; G211464; JOINED.
 DR PIR: A28875; TVCHET.
 DR PROSITE: PS00345; ETS_DOMAIN.1.
 DR PROSITE: PS00346; ETS_DOMAIN.2.
 DR PROSITE: PS00361; ETS_DOMAIN.3.
 DR HSP: P29578; ETS.1.
 DR TRANSFAC: T00115.
 KM PROTO-ONCOGENE: DNA-BINDING; NUCLEAR PROTEIN; ALTERNATIVE SPLICING.
 FT DNA_BIND 379 455
 FT CONFLICT 220 220 S -> C (IN REF. 2).
 FT CONFLICT 222 222 P -> R (IN REF. 2).
 SQ SEQUENCE 485 AA; 55021 MW; C58D8897 CRC32;

Query Match 15.2%; Score 272; DB 1; Length 485;
 Best Local Similarity 24.2%; Pseq. No. 6.4e-14;
 Matches 112; Conservative 42; Mismatches 109; Indels 200; Gaps 18;

65 MLYPEDSSMAAKP-----GASSREPEEP-----ECCPVDSQA--- 101
 2 KSHYKDTIGSTGPPPLAPGVWQASSCCEDPMPCRLQACPPSCCPMDMAVIOE 61
 101 -PAG-----SIDLYPGGLLEHSLSDQNSVYGEYLAKIETACKLLINTADPMSPSN 155
 62 VFGLEHSTDEKQADVPLTPSKKMSQALAKATSGFAEQGLIPIPDQMTETIV 121
 155 QKWLMTETHTYRLPPMKAFQE--TAGKELCMSEEPORSP-LGGDVLAHMDIKV-- 211
 122 KDMVMAHNEESL--KQVEFKCKMGALCLQKCTLELAFDVGDIIMHELETKE 179
 211 -----SAAMKKR-TSPALHY-----CASTE-----ESM----- 236
 180 EAKFPANGVNAAYPSRTSDYFISGLEHACVPEESEPSPFISTEYQILHPISEE 239
 240 -----TDS-----EV-----DSSCSQ----- 248
 246 LSLKTYENDPSYLVADPVDLSLOTDTFTIKQEVYVTDNMCKNASRKLGSQSFEST 299
 248 ----- 248
 300 ESYDCSRLTQSSQSSFSLSLRVPVDSQSEDPALPHNRKPKGTQVRYADAMN 359
 248 -----PTLMQFLKELLKPHSYGRFIRMLKKEGFIKEDSNQVAA 289
 360 KDPVYPAALAGTSSQPLQANQLE-LTSSQSSQFSTWG--DGMFFLSDPEVAR 417
 290 LMGIKRRPAMMYDKLSIRQYKCIIRPDISQILYQV 332
 418 RMCKRKKRPANMYEKLISGLRYTDKNKIHK-TAGRYVRYREV 459

RESULT 10
 FLII-MOUSE STANDARD; PRT; 452 AA.
 ID P26323;
 AC P26323;
 DT 01-MAY-1992 (REL. 22. CREATED)
 DT 01-MAY-1992 (REL. 22. LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 32. LAST ANNOTATION UPDATE)
 DE RETROVIRUS INTEGRATION SITE PROTEIN FLI-1.
 GN FLI OR FLI-1.
 OS MUS MUSCULUS (MOUSE).
 NC EURAYOYA, METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUHERIA;
 CC EUTHERIA; SCIROGNAHII; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 NC STRAIN-BALB/C; TISSUE-SPLEEN;

```

RA MEDLINE# 91257578.
RX BER-DAVID Y., GIDDENS E.B., LETWIN M., BERNSTEIN A.;
RT "Erythroleukemia induction by Friend murine leukemia virus:
RT "Erythroleukemia induction of a new member of the ets gene family, Flt-1,
RT "Ets family member, Flt-1, is a novel oncogene."
RN GENES DEV. 5:908-916(1991).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE# 93275657.
RA ZHANG L., LEWARCHANDEL V., ROMEO P.-H., BER-DAVID Y., GREER P.,
RA BERNSTEIN A.;
RT "The Flt-1 proto-oncogene, involved in erythroleukemia and Sying's
RT sarcoma, encodes a transcriptional activator with DNA-binding
RT sequence 8,198-91,031,193 on other Ets family members."
RC GENES DEV. 5:1001-1013(1991).
CC -1- FUNCTION: SEQUENCE SPECIFIC TRANSCRIPTIONAL ACTIVATOR. RECOGNIZES
CC THE DNA SEQUENCE 5'-C/CAAGG-3'.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BOTH HEMATOPOIETIC AND
CC NONHEMATOPOIETIC TISSUES.
CC -1- INDUCTION: SPECIFICALLY UP-REGULATED IN LEUKEMIC CLONES WITH
CC F-MULV INSERTIONS UP-STREAM OF THE FLT-1 LOCUS.
CC -1- LEUKEMIA: VIRUS (F-MULV)
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC -----
DR EMBL# X59421: G50975; -.
DR PIR# S17403: S17403.
DR MGD# MGI:95554; FLII.
DR PROSITE# PS00345; ETS.DOMAIN.1; 1.
DR PROSITE# PS00346; ETS.DOMAIN.2; 1.
DR PROSITE# PS00347; ETS.DOMAIN.3; 1.
DR PROSITE# PS00348; ETS.DOMAIN.4; 1.
DR HSP# 001543; 1.FLI.
DR TRANSFAC# T01408; -.
KW TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING; NUCLEAR PROTEIN;
KW PROTO-ONCOGENE.
FT DNA_BIND 281 361 ETS-DOMAIN.
FT SEQUENCE 455 281 CECACDD4 CRC32;

```

	Query Match	15.2%	Score 272	DB 1	length 452
	Best Local Similarity	25.6%	Pred. No. 58-14		
	Matches	Conservative	46	Mismatches 142	Indels 108
Qy	2	GSAPDLSVSPSPHLLLPDYVSRGLSEANANGCERPPDSSGPPAPPGC	-----ISA	57	
Dy	3	CTIEALSTVSDQSL-----PDAVCAALLKPKADPTAS--GSDPYGDPKIN	-----	50	
Qy	58	FLLSYEDMLVPESSMAAKPGASSRE-----PPEPPGCPYDSDAPGSLDVI	VG	111	
Dy	51	L-----PPOGELINQVYVANKETEDIMNGSSSPDQSVSKMVLGGSEANRN	101		
Qy	112	LT--LEHSLDQVSNVGVGLAKLEAQLKITADDPMPQSMQKLLLEHRYAL	169		
Dy	102	VASVMEKNGCPPPMKNTN-----RNVLPADPTLMTQEHVQWLEMAIKYGL	152		
Qy	170	PMGKA--FOELAGELCAWSEOF--RORSFLLGDVLYLAHL-----	207		
Dy	153	ELDSFQMDGELCKAKMNEEDFLAMSTVYRLSLHSLYLRSSLSLYATTSHT	202		
Qy	207	-----DIKSNAL-----	212		
Dy	213	RLNKKEDPSYDVRKANNNNNSGLNKSPLLGSGTQKGNKNDQPPDPVLTIG	275	271	

Qy	234	SWT05EVS05C050G1H04Q0F0E0K0L0R0H0Y0R0E0R0E0S0A0V0A0R0M0G	293
Qy	271	---SRLNPSGQ--IQMQLFLE--LLSDSNASCITM--ECTNREKMTDPEVARRNGE	323
Db	294	RANPANTDPSLESIQYKQKCEKDPDISOLAEYF	331
Db	324	RKSPNNYDKLSBALRYTDYDINMKTKH--GRKYAYNF	360
CC	11	RESULT	
CC	11	FL11-HUMAN	STANDARD: PRT: 452 AA.
CC	ID	FL11-HUMAN	001543.
CC	DE	01-JUL-1993 (REL. 26, CREATED)	
CC	DE	01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)	
CC	DE	01-NOV-1992 (REL. 35, LAST SEQUENCE UPDATE)	
CC	DE	FL11-ONCOGENE (EMBG TRANSCRIPTION FACTOR).	
CC	GN	FL11	
CC	OS	HOMO SAPIENS (HUMAN).	
CC	OC	ENKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:	
CC	NC	PRIMATES: CATARRHINI: HOMINIDAE: HOMO.	
CC	NC	(1)	
CC	RP	SEQUENCE FROM N.A.	
CC	RC	TISSUE: BONE MARROW;	
CC	RC	CELL: N.B.323	
CC	RA	DELAETTE O., HUMAN J., JOBERT I., DE JONG P., ROULEAU G.,	
CC	RA	PETER M., KOVAR H., JOHNETT J.,	
CC	RT	"Gene fusion with an ETS DNA-binding domain caused by chromosome	
CC	RT	translocation in human tumors."	
CC	RL	NATURE 359:167-169(1992).	
CC	RL	(2)	
CC	RP	SEQUENCE FROM N.A.	
CC	RC	MEDLINE: 93075640	
CC	RA	PARIS T.S., N., SETH A.,	
CC	RT	"The EMBL/FL1-1 gene: isolation and characterization of a new member	
CC	RT	of the family of human ETS transcription factors."	
CC	RL	CELL GROWTH DIFFER. 3:705-713(1992).	
CC	RL	(3)	
CC	RP	SEQUENCE FROM N.A.	
CC	RC	MEDLINE: 93007976.	
CC	RA	PRASAD D.D., BAO V.N., REDDY E.S.;	
CC	RT	"Structure and expression of human FL1-1 gene."	
CC	RC	CANCER RES. 52:5853-5859(1992).	
CC	RP	SEQUENCE FROM N.A.	
CC	RC	TISSUE: BLOOD;	
CC	RA	HEDLINE: 93176799.	
CC	RA	HOVARS R., MAY W., DENNY C., RASKIND W., MOORE E., MAKI R.A.,	
CC	RT	BECK E., KLEMSZ M.J.;	
CC	RT	"Human FL1-1 localizes to chromosome 11q24 and has an aberrant	
CC	RT	transcript in neuroblastoma."	
CC	RL	BIOCHIM. BIOPHYS. ACTA 1175:155-158(1993).	
CC	RL	(5)	
CC	RP	SEQUENCE FROM N.A.	
CC	RC	MEDLINE: 95230701	
CC	RA	LIANG H., MAO X., OLEINICKAR E.T., NETTESHEIM D.G., YU L.,	
CC	RA	MEADOWS R.P., THOMPSON C.B., FESIK S.W.;	
CC	RT	"Solution structure of the ets domain of FL1-1 when bound to DNA."	
CC	RT	NAT. STRUCT. BIOL. 1:871-875(1994).	
CC	CC	-1- FUNCTION: SEQUENCE SPECIFIC TRANSCRIPTIONAL ACTIVATOR, RECOGNIZES	
CC	CC	THE DNA SEQUENCE 5'CTCAAGGAG-3'.	
CC	CC	-1- SUBCELLULAR LOCATION: NUCLEAR.	
CC	CC	-1- DISEASE: A FORM OF SWING'S SARCOMA IS CHARACTERIZED BY A	
CC	CC	CHROMOSOMAL TRANSLOCATION T(11;22)(Q24;Q12) WHICH INVOLVES FL11	
CC	CC	AND EWS.	
CC	CC	-1- SIMILARITY: BELONGS TO THE ETS FAMILY	
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 DR EMBL: X67001: G32530: -
 DR EMBL: M98833: G182189: -
 DR EMBL: S45205: G57354: -
 DR EMBL: J11115: S87500: -
 DR PDB: 1JL1: 15-SEP-99.
 DR MIM: 193067: -SEP-99.
 DR PROSITE: PS00345: ETS_DOMAIN_1: 1.
 DR PROSITE: PS00346: ETS_DOMAIN_2: 1.
 DR PROSITE: PS50051: ETS_DOMAIN_3: 1.
 DR TRANSFAC: PF00178: Ets: 1.
 DR TRANSFAC: PF00179: Ets: 1.
 KW TRANSCRIPTION REGULATION: ACTINATOR: DNA BINDING: NUCLEAR PROTEIN:
 KW PROTO-ONCOGENE: CHROMOSOMAL TRANSLOCATION: 3D-STRUCTURE.
 FT DNA_BIND 281 361
 FT CONFLICT 69 69 E -> V (IN REF. 4).
 FT CONFLICT 77 77 MISSING (IN REF. 4).
 FT CONFLICT 130 130 W -> A (IN REF. 4).
 FT CONFLICT 133 133 W -> V (IN REF. 4).
 FT CONFLICT 323 323 Y -> Q (IN REF. 3 AND 4).
 FT CONFLICT 391 391 Y -> Q (IN REF. 3 AND 4).
 FT CONFLICT 426 426 MISSING (IN REF. 2 AND 4).
 SQ SEQUENCE 452 AA: 50982 MW: 19247677 CRC32.

Query Match 15.18: Score 270: DB 1: Length 452:
 Best Local Similarity 23.98: Pctd No. 8,3e-14: Idels 108: Gaps 17:
 Matches 103: Conservative 50: Mismatches 137:
 DB 2 GSASGSLSVSPSHLLLPPTVSRGTGKAAAGVGLERDMPSPAPPREG---ISA 57
 DB 3 GTKRALSVSDQSL-----PDSVGAHAHLERADMTAS--GSPDYGQPKRNP 50
 QY 56 FYLSTFDMKLPEDSSNAKAFQSSREE-----PEEEDQCPYDQAPAGSLDYVGG 111
 DB 51 L-----PQGEWINGPVRYNKKEDHNNSSNESTYDCSV-----SKCKLIVGG 95
 QY 112 LT-----LEHSLDEVQSNVGEVLDIEFTACKLNTITADPMDSNSVOKMLWTE 163
 DB 96 ESNPANNYSYMEKNENPPPPMTNTE-----RVIYPADPTLMTQEHVROMLEMAI 146
 QY 164 HOYRLPRMGKA-FOELACKELCKASEQERQSRFL-GDVTLANH----- 207
 DB 147 KEYSLEIDTSTFONMDKELCKNNKDLRLRITLNTLVELSHLSLSTLESSLIANTTS 206
 QY 207 -----DINKSAAMKRRSP-----GAHYCASTSEF----- 234
 DB 207 HDSOSRLSVEDPSYSDSVSRGAGANNMNSLKNKSPPGAQOTISKNTQSORPQYCI 266
 QY 234 SWTDSFVDSGSSGQPIHLKQFTKELLKPKSYGFTIRLKKRGGFPIEDSAQVVARLWGI 293
 DB 267 GPTSRILANPGSQ-IQMOFLLE-LVSSNANSCITL-BGNNEFKMDPDEVANRWGG 323
 QY 294 RKNRPANNYDKLSRSIRQYKGIIRRPDISRLQYVGG 331
 DB 324 RKSRRNNYDKLSRLALRYVDKNIIMTVH-GKRYAYKE 360

RESULT 12
 ETV6_MOUSE STANDARD: PRT: 485 AA.
 ID ETV6_MOUSE
 AC P97360:
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DT ETS-RELATED PROTEIN TEL (ETS TRANSLLOCATION VARIANT 6).
 CN ETS-RELATED PROTEIN TEL (ETS TRANSLLOCATION VARIANT 6).
 OS MUS MUSCULUS (MUSE)
 OC EMBRYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 CC EUCARYOTA: SCUROGNATHI: MURIDAE: MORINAE: MOS.
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J:
 RC BERNARD O.:
 RC SUBMITTED (DEC-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- SWISSPROT BELONGS TO THE ETS FAMILY.
 CC -1- SWISSPROT BELONGS TO THE ETS FAMILY.
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 CC or send an email to license@lsb-sib.ch)
 CC EMBL: Y07915: E274398: -
 DR MGI: MGI:109316: ETV6.
 DR PROSITE: PS00345: ETS_DOMAIN_1: FALSE_NEG.
 DR PROSITE: PS00346: ETS_DOMAIN_2: 1.
 DR TRANSFAC: PF00178: Ets: 1.
 DR HSP: 001543: TEL: 1.
 KW NUCLEAR PROTEIN: DNA BINDING.
 FT DNA_BIND 335 416
 FT SEQUENCE 485 AA: 56405 MW: 12475087 CRC32.

Query Match 14.98: Score 265.5: DB 1: Length 485:
 Best Local Similarity 21.98: Pctd No. 2e-12: Idels 223: Gaps 15:
 Matches 98: Conservative 47: Mismatches 80:
 DB 75 AKAFASREE-----PEEEDQCPYDQAPAGSLD--VGGILTEPHSLQVQSW 126
 DB 2 SEIPAGSSITKQERISITPPESP-----VASHSSPTLVHTVPRALREEDSIH----- 51
 QY 127 VGEVLDIEFTACKLNTITADPMDSNSVOKMLWTEQYRLPRKANVDELACKELCM 186
 DB 51 -----LPTHLRL-----QPIYSRDOVQVLAHNEFSLAPTEENKFEVCKALLL 98
 QY 187 SEQCFRQSRPLGADYLR--AHLDIKMSAAMKERTS-----FG----- 223
 DB 99 TKEDFRVNSHSGDYLTELQHT-----LKRQSRMLSPFEFGDSIHTRPEVLIH 150
 QY 223 -----AIHYCASTSE----- 233
 DB 151 QNHEDNCVQRTPTPAESVHNHPTELLHNPSPITTHNRPSPDEQQRQSRSLDM 210
 QY 233 -----ESWTDS----- 239
 DB 211 SRLSPVEKQAPFADQENNHQETVPLSVPEVNNHCLPSSPOEGRVYOLMPSFINHP 270
 QY 239 -----PNDSSCS-----GQPIH----- 251
 DB 271 LILNPRSHSVDFKQSRNSEDQKNECKRPILNSHRDVALYLHIYNSMPEEHNAPIC 330
 QY 331 -----LMOFLKELLKPKSYGFTIRLKKRGGFPIEDSAQVVARLWGIIRKRPANNYD 304
 DB 331 IACKELMDYVQ-LVSSDRIENFTFRKESKSLPIVDNGLARLGMHNNKNTMYER 389
 QY 305 LRSRSIRQYKGIIRRPDISRLQYVGG 332
 DB 390 MSRLALRYVLTIR-PPQGRILPRFM 416

RESULT 13
 ETV6_MOUSE STANDARD: PRT: 452 AA.
 ID ETV6_MOUSE
 AC P41212:
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DT ETS-RELATED PROTEIN TEL (ETS TRANSLLOCATION VARIANT 6).
 CN ETS-RELATED PROTEIN TEL (ETS TRANSLLOCATION VARIANT 6).
 OS MUS MUSCULUS (MUSE)
 OC EUCARYOTA: SCUROGNATHI: MURIDAE: MORINAE: MOS.
 RN [1]

CC EXTREMITY: P54 AND P68.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC
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CC
CC EMBL: M22462; G211793; .
CC DR EMBL: X13029; G63180; .
CC DR EMBL: X13029; G63180; .
CC DR PIR: A31285; TWCHPE; .
CC DR PIR: S07625; S07625.
CC DR PIR: S29132; S29132.
CC DR PROSITE: P800345; ETS_DOMAIN_1; 1.
CC DR PROSITE: P800346; ETS_DOMAIN_2; 1.
CC DR PROSITE: P50061; ETS_DOMAIN_3; 1.
CC DR HSP: P21576; Ets; 1.
CC DR HSP: P21576; Ets; 1.
CC DR TRANSFAC: T00114; .
CC
CC PHOTO-ONTOGENE: DNA-BINDING; NUCLEAR PROTEIN; ALTERNATIVE SPLICING;
CC PHOSPHORYLATION.
CC
CC DOMAIN 54 135 POINTED.
CC ETS_DOMAIN.
CC DNA_BIND 335 415
CC MOD_RES 38 38 PHOSPHORYLATION (BY MARK) (BY
CC CONFLICT 117 117 R 22 A IN REF. 3).
CC
CC SEQUENCE 441 AA: 50326 MW: 73453953 CRC32:
SO

Query Match 14.18; Score 292.5; DB 1; Length 441;
Best Local Similarity 24.08; Pred. No. 1,8e-12;
Matches 96; Conservative 38; Mismatches 89; Indels 177; Gaps 15;
DB 21 IDLFFSPDMECADVPLLPSSKEDMSQALKAFTGFAEERKRLGPRDQVTEIYHDM 80
OY 159 LMTFHOYRLPPMKRFOE-LAGEKELCAHSEDFORSP-LGGDYLAHNDIMK- 211
DB 81 VMANVNEESL-KGVDFORCKMGALCALGCEGFELEKRDYDGLIMHELEIIOREAR 138
OY 211 - - - - -SAAMKER-TSPQATY- - - - -CASTS- - - - -ESN- - - - - 236
DB 139 PYBANGNAAPRESRTSDYFISYDGHOCVPSFSESRITBISYOTLPISSSEILS 198
OY 236 - - - - -TDS- - - - -EV- - - - -DSSCSGO- - - - - 248
DB 199 LKENDYFVYLKPDVOTDLSQTDYFTIKQEVYTPDNCKMGASRNGLAGODSFESIEBY 258
OY 248 - - - - -TDS- - - - -EV- - - - -DSSCSGO- - - - - 248
DB 259 DSCDELTOSSMSOSSFOSLORVPISDFSDPDAALPNHKKRGTREYVADDAOMKXK 318
OY 248 - - - - -PIHLMQLEKLLPHSGGRIRIMNKGKFIKEDSAQVARELNG 292
DB 319 PYIPIAALAGTSGSGLDQMLEL-LINDSCOSFISMTG-DOMEKFLSDPEVARENG 376
OY 293 IKRRPNAMVYKXSSISROYKXGILKPKDLSORLATQVY 332
DB 377 KKKKKPMNVYKESLRCGLRYTDKNILHK-TGGRVRYEY 415
RESULT 15
ID ETS2B_XENLA STANDARD; PRT: 472 AA.
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE C-ETS-2B PROTEIN.
OS XENOPUS LAEVIS (AFRICAN CLAMPED FROG).
OC METAZOA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
CC MESOCHORDATA; FILOIDEA; PIPOIDEA; XENODODINAE; XENOPUS.
RN [1] TISSUE-OVARY.
RC SEQUENCE FROM N.A.
RX MEDLINE: 90356411.
RA WOLFE C.M., STEIGLER P., BALTZINGER M., MEYER D., GHYSOUEL J.,
RT "TITRATION OF TWO DIFFERENT C-ETS-2 PROTO-ONCOGENES IN XENOPUS
RL NUCLEIC ACIDS RES. 18:4603-4604(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-OVARY.
RX MEDLINE: 92088972.
RA WOLFE C.M., STEIGLER P., BALTZINGER M., MEYER D., GHYSOUEL J.,
RT "CLONING OF THE XENOPUS C-ETS-2, AND EXPRESSION OF TWO XENOPUS LAEVIS C-ETS-2
RT PROTOONCOGENES", and expression of two Xenopus laevis c-ets-2
RL CELL GROWTH DIFFER. 2:447-456(1991).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC
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CC
CC EMBL: X53635; D64621; .
CC DR PROSITE: P800345; ETS_DOMAIN_1; 1.
CC DR PROSITE: P800346; ETS_DOMAIN_2; 1.
CC DR PIR: P50061; ETS_DOMAIN_3; 1.
CC DR PIR: P500178; Ets; 1.
CC DR HSP: P14921; 2STW.
CC
CC DNA-BINDING; NUCLEAR PROTEIN; ETS-DOMAIN.
CC DNA_BIND 366 446
CC SEQUENCE 472 AA: 35928 MW: 19650684 CRC32:
SO

Query Match 14.08; Score 290; DB 1; Length 472;
Best Local Similarity 22.98; Pred. No. 3.1e-12;
Matches 92; Conservative 35; Mismatches 91; Indels 184; Gaps 15;
DB 108 VEGGLTEHS- - - - -LEQVSNVGVGLKD- - - - -IETKCLNTADPMDWSSN 154
OY 52 VFGVDSPIDSSCELPALPSCANVNSQALKDTNCFNEKRP-LGIRNPMLNDNM 110
OY 155 VQMLMTFHOYRLPPMKRFOE-LAGEKELCAHSEDFORSP-LGGDYLAHNDIMK- 208
DB 111 VQMLVNAKERSLENYN-FQRTFLMGHCLCSIGREKFLALAPDVGIIIMHELEKMA 168
OY 168 - - - - -IKNSAAMKERTSP- - - - - 222
DB 209 EYGEAGEPTIDHNSDLSNMDNSLFTNADLOCAQVHNPKNGWYNDKCSVPTGO 228
OY 222 - - - - -GAHYCASTE- - - - - 233
DB 229 TLINKEFOYTPSCNLSAAYVNPASDFAHSHWVLLNSLNGKLDYDGSOSTES 288
OY 233 - - - - -ESWTDSB- - - - -VSSC- - - - - 245
DB 289 FSTESLHNSWSSLDVNDQRPISDFSEKNGTCLAKQPKSFNDIOTDKCEPAELD 348
OY 245 - - - - -SGCPILHMQLEKLLPHSGGRIRIMNKGKFIKEDSAQVAREL 290
DB 349 KVPYFASILAAGTSGS-PIDLMQLEL-LINDSCOSFISMTG-DOMEKFLSDPEVARE 405

RESULT 2
ERG_HUMAN STANDARD: PRT: 462 AA.
ID ERG_HUMAN
AC P11308.1989 (REL. 11, CREATED)
DT 01-JUN-1989
DE 15-DEC-1988 (REL. 31, LAST SEQUENCE UPDATE)
DE TRANSCRIPTIONAL REGULATOR ERG (TRANSFORMING PROTEIN ERG) (ERG-2/ERG-1).
GN ERG.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
NC
RP SEQUENCE FROM N.A.
RA MEDLINE: 87263429.
RA Rao V.N., PAPAS T.S., SHYAM E., REDDY P.;
RT "erg, a human ets-related gene on chromosome 21: alternative
RT splicing, polyadenylation, and translation.";
RT SCIENCE 237:635-639(1987).
RN
RS
RT SEQUENCE OF 100-462 FROM N.A.
RX MEDLINE: 87317608
RX REDDY E.S.P., RAO V.N., PAPAS T.S.;
RT "The erg gene: a human gene related to the ets oncogene.";
RT PROC. NATL. ACAD. SCI. U.S.A. 84:6131-6135(1987).
RN
RP CHROMOSOMAL TRANSLOCATION.
RX MEDLINE: 94356859.
RX DUNN J., PAPERSON L., JACAC N., VIOLA M.V.;
RT "ERG gene is translocated to 12p13 in human
RT CANCER GENET. CYTOGENET. 76:19-22(1994).
RN
RP CHROMOSOMAL TRANSLOCATION.
RX MEDLINE: 94243799.
RX ACHIRMAN H., SHIMIZU K., HAYASHI Y., OHKI M.;
RT "The human ets-related protein gene, TLS/PUS, is fused to ERG in human
RT myeloid leukemia.";
RT CANCER RES. 54:2865-2868(1994).
CC -1- FUNCTION: ACTS AS A TRANSCRIPTIONAL ACTIVATOR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- DISEASE: A FORM OF ACUTE MYELOID LEUKEMIA (AML) IS CHARACTERIZED
CC BY A CHROMOSOMAL TRANSLOCATION T(16;21)(p11;q22) WHICH INVOLVES
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC
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CC
CC EMBL: M17254; GI82187; -
CC EMBL: M21535; GI82185; -
CC PIR: A29515; TVHDEG.
CC MIR: 165080.
CC PROSITE: PS00345; ETS_DOMAIN_1; 1.
CC PROSITE: PS00345; ETS_DOMAIN_2; 1.
CC PFM: PFO0178; Ets; 1.
CC HSP: 001543; 1EL1.
CC TRANSFAC: T00265; -
CC TRANSFAC: T00266; -
CC TRANSCRIPTION REGULATION: ACTIVATOR; NUCLEAR PROTEIN; DNA-BINDING;
CC TRANSFORMING PROTEIN; ALTERNATIVE INITIATION; PROTO-ONCOGENE;
CC CHROMOSOMAL TRANSLOCATION.
CC TRANSFORMING PROTEIN ERG-2.
CC CHAIN 100 462
FT DNA_BIND 294 374 TRANSFORMING PROTEIN ERG-1.
SQ SEQUENCE 462 AA: 52031 MW: CECQD2B CMC32;

Query Match 16.8%; Score 300.5; Db 1: Length 462;
Local Similarity 26.7%; Pred. No. 3.7e-16;
Matches 103; Conservative 46; Mismatches 118; Indels 117; Gaps 17;
Oy 45 PEPPTPEGGASAF-----YLSYDPL-----YEDSSNAKPPASNE 84
Db 6 PPAAHKEALSVSDSIPECAVGHPLATATSSSDYQISMSGRVPODMS 65
Oy 85 EPP-----EEPECPVDSIAPASISDLP---GELTLESHSLQVQ 123
Db 66 PPAPATITMCPQVQVQNSRNSDSCSVAKGKGVSPVGVNNGVYEEKHH--PP 123
Oy 124 SWVGEVLMKDIETACKLITNPDMQSPNSQVCKLITENQVITLPFG-RAFOELAGE 182
Db 124 NNTNE-----RAYVPADETMTSDHVMQVLEMAVVEIGLDPVNLIFQVIGKE 174
Oy 175 LCAWSEDFRQSP-IGGVYLAHL-----DIKS----- 212
Db 175 LCAWTFKQDFVSTYADILSHLYRETPLPLHLSDDVDALONSPLMAHANTDLP 234
Oy 212 -----AAW-----MKERTSGVATKCAHSE-----SWTSEVDSGCS 245
Db 235 YEPFRHSAVTSQHPTPOSKAAPSPSTV---PKTEQNPQLPQVLIQPTSKMLNPGS 291
Oy 246 GQPIHLMQFLKELIKPHSGYGFHMLKKKGIFEDSAQVAFALMGIRKNPANNYL 305
Db 292 QG IOLMPGLE-LTSDSSNSGCTH-EGTNEFRMTDDEAVRMRGRSKPNANNYDL 348
Oy 306 SRSIRQYTKGIRKPDISQLAYOP 331
Db 349 SVALRYDYKNIMTVA-GKRYAYKE 373
RESULT 3
ERG_DROME STANDARD: PRT: 464 AA.
ID ERG_DROME
AC Q04688.
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DE 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE TRANSFORMING PROTEIN D-ERG.
GN ERG270.
OS DROSOPHILA MELANOGASTER (FRUIT FLY).
OC EUKARYOTA; METAZOA; ARTHROPODA; TRICHERA; HEXAPODA; INSECTA;
OC PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYROIDEA.
OC DROSOPHILIDAE; DROSOPHILA.
RN
RP SEQUENCE FROM N.A.
RX MEDLINE: 8066781.
RX WHEATON R., XIE Y.S., SWYTH F., PAPAS T.S., WATSON D.K., SCHULTZ R.A.;
RT "The molecular characterization and evolution of Drosophila
RT ets proto-oncogene-related gene of Drosophila.";
RT ONCOGENE 7:2471-2478(1992).
RN
RS
RT SEQUENCE OF 323-463 FROM N.A.
RX MEDLINE: 91319397.
RX WHEATON R., SCHULTZ R.A., PAPAS T.S.;
RT "The ets proto-oncogene-related gene of Drosophila: sequence,
RT expression and evolutionary comparison.";
RT ONCOGENE 6:1175-1183(1991).
RN
RS
RP SEQUENCE OF 298-449 FROM N.A.
RX MEDLINE: 92249640.
RX WHEATON R., BUNTING M., KARIM F.D., THUMMEL C.S.;
RT "The structure and characterization of five Drosophila genes that encode
RT an ets-like protein containing a conserved domain.";
RT DEV. BIOL. 151:176-180(1992).
RN
RP
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC
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 CC EMBL: 66295; G7913;
 DR EMBL: X58481; G7911; ALT.MIT.
 DR EMBL: M88471; G553086;
 DR PIR: S24300; S24300.
 DR PIR: S28822; S28822.
 DR PIR: S37616; S37616.
 DR FLYBASE: Fgmd004510; Ets97D.
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_3; 1.
 DR PFM: PFM0178; Ets; 1.
 DR HSP: 000423; IWC; 1.
 DR TRANSFAC: T02085;
 DR DNA-BINDING: NUCLEAR PROTEIN; ETS-DOMAIN.
 DR DNA_BIND 346 426
 FT SEQUENCE 464 AA; 5265 MW; A75B9B7A CRC32;
 SQ
 Query Match 16.5%; Score 294; DB 1; Length 664;
 Best Local Similarity 29.1%; Pred. No. 1,26-15;
 Matches 92; Conservative 52; Mismatches 116; Indels 56; Gaps 12;
 64 DMLPDESSMAKAPGASSREPEPECCVVIDSQAPASIDLVPQGLTEHSLEQVO 123
 118 DVLKPTDALLALAEVYGLPPTASQ-----KSSSESPFKTPPLKRNKEDSEESVE 173
 124 SMVGEYLK-DITACK-----LNTADPMDSPSNQKLLTPEHKEITPPGKAPQEL 178
 174 GADVPLVLMWLSKFKREQIRLKIPRANEMTHAIVLYLMAVKEQELGINSMDQM 233
 179 ACKELCANSEDFRQSRPLG-GDVLAHMLDIMSAAAM-----KRRSP----- 222
 234 NQDELCAHHEEFNOKLPDPNFIEMHQLLKECFVSVAKRAEQRKPKRPLMSAN 293
 292 -----GAT-----HICASISESWTDS-----EYDSCSGPIHLMQFL 295
 294 SITSNGSGLSQRIMAKSYKSDSEITSSMPNTTIGSNGQ-VOLMPEFL 352
 296 KELLKPHSGYGRIFMLNKKGIPIEDSAQVAVLWLRKRNPNANVDLSRSIRYKK 315
 333 LE-LITCEHTDVIEMVGTG-GEFLTDDPVALVGEKKRPNMERTLSALRYTGD 410
 316 GIKRPDISQRLVYQF 331
 411 DMSISVS-GKRFNFK 425
 DB
 RESULT 4
 ID ERG_CHICK STANDARD: PRT: 478 AA.
 AC 090837;
 DT 15-DEC-1998 (REL. 37, CREATED)
 DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE TRANSCRIPTIONAL REGULATOR ERG.
 DE ERG (ERG) (ERG)
 OS GALLUS GALLUS (CHICKEN)
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAUROIA; AVES;
 CC NEOMETHIAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SPLEEN;
 RC MEDLINE: 95329425.
 RA DHORAHN P., DEWITTE F., DESBIENS X., STEHELIN D.,
 RA DUTEROUX-COULLAUD M.,
 RT "Methodical expression of the chicken erg gene associated with

RT precartilaginous condensation and cartilage differentiation";
 RL MCH. DEV. 50:17-28(1995).
 CC -1- FUNCTION: ACTS AS A TRANSCRIPTIONAL ACTIVATOR.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MESODERM- AND, TO A LESSER
 CC EXTENT, IN ECTODERM-DERIVED TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
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 CC EMBL: X77159; G790440;
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_3; 1.
 DR PFM: PFM0178; Ets; 1.
 DR TRANSFAC: T02085;
 DR DNA-BIND 310 390
 FT SEQUENCE 478 AA; 53513 MW; CFEA9D2C CRC32;
 SQ
 Query Match 16.4%; Score 292; DB 1; Length 478;
 Best Local Similarity 26.9%; Pred. No. 1,86-15;
 Matches 98; Conservative 39; Mismatches 113; Indels 114; Gaps 14;
 67 YPEDSSMAKAPGASSREPEPECCVVIDSQAPASIDLVPQGLTEHSLEQVO 108
 41 YQTSKASFRVPOQDMLSGPNAVITMECPKPNVONSRRNSDSCSYAKGKAVSSDNV 100
 109 P---CGLTLEHSLQNOVWGVGLKDIETACKLNTADPMDSPSNQKLLTPEHKEIT 165
 101 GANNQYMEKHI--PPNNTTNE-----RNVYPADTLMSTDHVHQLLEMAVKE 149
 166 YELPFGK-KARDELAKELCANSEDFRQSRP-LAGDVLAHL-----DIT 209
 150 YGLPDVILLNINQIKELCKTKDQFORLPSYADLLSHLRYLRETPPLMLTSDVD 209
 210 K-----SANKERTSPALHICASTS-----EESV----- 236
 210 KALNSRRLMHANMGATFIPNIVYEAELQRTTRPDLVQANRANVTSHSPQS 269
 236 -----DSEVDSGSGPIHLMQFLKELLKPHSYGA 267
 270 KATPSSSTVTEKEDRPOLDYQIIGLPTSSRLAPGSGQ-TOLMPEFLLE-TLSDSNSR 327
 268 FIRMNKEGIFRIEDSAQVAVLWLRKRNPNANVDLSRSIRYKKGIKRPDISQR 327
 328 CLTM-EGTNGEFTMDPDEVANNGEKSNKNTADKLSALKTIDKNTMYH-GKRI 385
 328 AYRF 389
 DB
 RESULT 5
 ID GABA_HUMAN STANDARD: PRT: 454 AA.
 AC 030293;
 DT 03-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE GABA BINDING PROTEIN ALPHA CHAIN (GABR-ALPHA SUBUNIT) (TRANSCRIPTION
 DE FACTOR EATF1-60) (NUCLEAR RESPIRATORY FACTOR-2 SUBUNIT ALPHA).
 OS HOMO SAPIENS (HUMAN).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]

Db 259 VPLPSEKEMMSALKATFSGFAKEOORLGIPIPDQOETETIVADYVMAVNFSL--K 316
 172 GAAFOE--LACKELCANSEEDFORPSR-LGGDVLHAHLDIKR-----SAAWK 216
 Db 317 GADFOCKMNAALCALGRCEFLAALDEPGLMEHLLELOKEAARPRANGVNAIPE 316
 317 ER-TSPARHY-----CASTSE-----ESV----- 226
 Oy 217 ER-TSPARHY-----CASTSE-----ESV----- 226
 Db 377 SRVTSDFISYCIENACVPPSEFSESEFTESYOTLPIRISSEELSLKXENDPVILR 436
 Oy 236 ---TDS-----EV---DSSCSGQ----- 248
 Db 437 DPVOTSLDITDFTTKOEVYTPDNCKGVRVSGKLGSDSFESIYSQDCLTOSMSQ 496
 Oy 248 ----- 248
 Db 497 SPSOSLOARPSYDSFSDSEYPAALPHKPRGPIPDYVDRADMDKDPVYPAALAGTIG 556
 Oy 248 ---PHLMQFLKELLKPSHVGRIEMKKEIGESAGVAVLAMIIRKRNPMYNDKL 305
 Db 557 SGILOLQFLE-LITDKSCOSFISMG-DOMEKFTLSDPEVARMGRKRNKPMQYEL 614
 Oy 306 SRSIRQYKKGIIIRKPDISQRLVYOFY 332
 Db 615 SRGLVYIDKNIYHK-TAGKRYVIRFY 640

RESULT 7
 CABLA_MOUSE STANDARD: PRT: 454 AA.
 ID CABLA_MOUSE 000422;
 AC 01-DEC-1992 (REL. 24, CREATED)
 DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATED)
 DT 01-DEC-1992 (REL. 36, LAST ANNOTATION UPDATED)
 DT 01-DEC-1998 (REL. 36, LAST ANNOTATION UPDATED)
 DB 361 BINDING PROTEIN ALPHA CHAIN (GAMP-ALPHA SUBUNIT).
 GN CABLA
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; MUS.
 RN 111
 RA SEQUENCE FROM N.A.
 RX MEDLINE: 91343912.
 RA LAMARCO K., THOMPSON C.C., BYERS B.P., WALTON E.M., MCKNIGHT S.L.;
 RT Identification of Ets-and mocsn-related subunits in Gα binding
 RL SCIENCE 253:769-792(1991).
 RN 121
 RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 320-320.
 RX MEDLINE: 98128030.
 RA BOTSCHLOAR A.H., PIPER D.E., DE LA BROUSSE F.C., MCKNIGHT S.L.,
 RX WOLBERGER C.;
 RT The structure of CABLA/alpha/Decla: an ETS domain-ankyrin repeat
 RL SCIENCE 279:1037-1041(1998).
 CC -1- FUNCTION: TRANSCRIPTION FACTOR CAPABLE OF INTERACTING WITH PURINE
 CC -1- RICH REPEATS (GA REPEATS).
 CC -1- SUBUNIT: HETERODIMER OF TWO ALPHA AND TWO BETA SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- TISSUE SPECIFICITY: BRIOGUTS.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
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 CC or send an email to: license@sib-sib.ch).
 DR EMBL: M74513: G193383: -
 DR PIR: A40858: A40858:
 DR PDB: 1AWC: 18-MAR-98.

DR MGD: MGI:95610: CABLA.
 DR PROSITE: PS00345: ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346: ETS_DOMAIN_2; 1.
 DR PROSITE: PS50061: ETS_DOMAIN_3; 1.
 DR PFAM: PF00178: Ets; 1.
 DR TRANSFAC: T00298; -
 DR TRANSFAC: T00422; -
 KW TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN; 3D-STRUCTURE.
 FT DNA BIND 320
 SO SEQUENCE 454 AA; 51363 MW; C3845F76 CRC32;

Query Match 15.5%; Score 277; DB 1; Length 454;
 Best Local Similarity 28.8%; Pred. No. 2,46-14;
 Matches 83%; Conservative 43; Mismatches 116; Indels 46; Gaps 9;

Oy 78 PASSREPERPEPOCPYDSOAPGSLDVPGLTEEMSLSEORELSOMVGEVLDKETA 137
 Db 136 PDMHAEALALVEAOYI-----TLDRKHTITSDISQYRWMA--ALEGYRKE 176
 Oy 138 CKLMLTADPMQSPENYOKMLTETQYRLPRPKAARQELKCLANSEEDFORSPFL 197
 Db 177 QELDILPIPIRSTQYLVLMVNNKESWTMDITLTLNISRELSLSMDDEFRVP- 236
 Oy 198 GSDVLAHLDIKSAAWKER-----TSQAHLICASTS----- 232
 Db 236 RGEILMSHELLKRYVLSODQOMLEYITDQPIQIYASVPRAPIPTIKYINSAAK 295
 Oy 232 -RESVTDSEVSDSCSGO-----PHLMQFLKELLKPSHVGRIEMKKEIGFRTIDS 284
 Db 236 VDSRPSRIGEDRSRPNRTGNGOIQLOFLELTDLRDARD-CISVGDG-GEFYLNP 353
 Oy 285 AQAARLGIIRKRNPMYNDKLSIRQYKKGIIIRKPDISQRLVYOFY 332
 Db 354 ELVAMNGRKNRMTYKMTLSALRTITDMDICVNO-GARVYIKV 400

RESULT 8
 FLII_XENLA STANDARD: PRT: 453 AA.
 ID FLII_XENLA 041157;
 AC 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATED)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATED)
 DB 171 PROTEIN INTEGRATION SITE PROTEIN FLII-1 HOMOLOG.
 GN FLII
 OS XENOPUS LAEVIS (AFRICAN CLAMMED FROG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
 OC MESOARTHRODIA; DIPLODEA; PIPIDAE; XENOPODINAE; XENOPUS.
 RN 111
 RA SEQUENCE FROM N.A.
 RX MEDLINE: 94205844.
 RA BEHREND D., WOLBERGER P., STIEGLER P., SENAN F., BEHREND N.,
 RT "X1-Fl1, the Xenopus homologue of the fl1-1 gene, is expressed during
 RT embryogenesis in a restricted pattern evocative of neural crest cell
 RT distribution.";
 RL MECH. DEV. 44:109-121(1993).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYOGENESIS.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
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 CC or send an email to: license@sib-sib.ch).
 DR EMBL: X66973: G505487: -
 DR PROSITE: PS00345: ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346: ETS_DOMAIN_2; 1.

01-MAY-1992	(REL. 22, LAST SEQUENCE UPDATE)
01-NOV-1995	{REL. 32, LAST ANNOTATION UPDATE}

T	01-MAY-1992 (REL. 22, CREATED)
T	01-MAY-1992 (REL. 32 LAST SEQUENCE NUMBER)

DE RETROVIRAL INTEGRATION SITE PROTEIN FLI-1.
 GN FLI1 OR FLI-1.
 OS MUS MUSCULUS (MOUSE).
 CC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 CC RODENTIA: SCIRIACANTHRI: MURIDAE: MURINAE: MUS.
 RN
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-SPLEEN;
 RC REF: 157521
 RA BEY-DAVID J., GIDONS E.B., LETWIN K., BERNSTEIN A.;
 RT "Erythroleukemia induction by Friend murine leukemia virus:
 RT Inertional activation of a new member of the ets gene family, flt-1,
 RT closely linked to c-ets-1.";
 RL GENES DEV. 5:908-918(1991).
 RN
 RN [2]
 RN CHARACTERIZATION.
 RA MEDLINE: 93273657.
 RA BERNSTEIN A., LEONARDEL V., ROMEO P.-H., BEN-DAVID Y., GREEN P.,
 RA "The flt-1 proto-oncogene, involved in erythroleukemia and Ewing's
 RA sarcoma, encodes a transcriptional activator with DNA-binding
 RT specificities distinct from other Ets family members.";
 RL ONCOGENE 8:1621-1630(1993).
 CC
 CC -1- FUNCTION: SEQUENCE SPECIFIC TRANSCRIPTIONAL ACTIVATOR. RECOGNIZES
 CC -1- THE DNA SEQUENCE 5' C[CA]GGAAGT-3'.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- TISSUE: BONE MARROW; BLOOD; LYMPH; THYMUS; SPLEEN; THYROID;
 CC -1- NONHEMATOPOIETIC TISSUES EXPRESSED IN BOTH HEMATOPOIETIC AND
 CC -1- INDUCTION: SPECIFICALLY UP-REGULATED IN LEUKEMIC CLOVES WITH
 CC -1- F-MULV INSERTIONS UP-STREAM OF THE FLI-1 LOCUS.
 CC -1- DISEASE: INVOLVED IN ERYTHROLEUKEMIA INDUCTION BY FRIEND MURINE
 CC LEUKEMIA VIRUS (F-MULV).
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC
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 CC
 CC EMBL: 554921; G50875.
 CC PIR: S17403; S17403.
 DR MCD: MGI:95554; FILL.
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_3; 1.
 DR PFM: PF00178; ETS; 1.
 DR HSP: P01543; FTL; 1.
 DR TRANSFAC: T01408; .
 DR PROSCRIPTION REGULATION: ACTIVATOR: DNA-BINDING; NUCLEAR PROTEIN;
 DR PROSCRIPTION REGULATION: ACTIVATOR: DNA-BINDING; NUCLEAR PROTEIN;
 DR PROSCRIPTION REGULATION: ACTIVATOR: DNA-BINDING; NUCLEAR PROTEIN;
 FT DNA BIND 281 361 ETS DOMAIN.
 FT SEQUENCE 453 AA; 51002 MW; CECACDQI CRG32;
 SO
 Query Match 15.2%; Score 272; DB 1; Length 452;
 Best Local Similarity 25.6%; Pred. No. 5,86-14;
 Matches 102; Conservative 46; Mismatches 142; Indels 108; Gaps 16;

Oy 170 PIGRA-FOELAGELCAMSEPOF-NORSLPGDVAHL----- 207
 Db 153 EIDISFFONMGKELCCKNKEDEFLAITSAYTEVLLSHLSYRESSLLAYMTSHTDSS 212
 Oy 207 -----DIKSAW-----MKERTSFOAHTCASTSEE 233
 Db 213 RANKEDEPSTSVRRGAMNNNSKLSPGLSGTNGKNTEDPDPOLLGPT-- 271
 Oy 234 SMTSEYDSSCGCPHKKPILKELLFHSHYGRFLPKKEKIFETDSAGVAMIG 293
 Db 271 -----SLRAPSQD-IQMOFILE-ILSDSANMSCTV-DGTNEFPMDDDEVARHGE 323
 Oy 294 RKNRPANVDLSRSIRQYKFGIRPDISOLVYOF 331
 Db 324 RSKRPNNYDKLSRALRYTDKNIMTRVH-KRRVAFK 360
 RESULT 11
 FLI1 HUMAN STANDARD; PRT; 452 AA.
 ID FLI1 HUMAN
 AC 001543;
 DT 01-JUL-1993 (REL. 26, CREATED)
 DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE FLI-1 ONCOGENE (ENGB TRANSCRIPTION FACTOR).
 DE
 DE FLI1, SAPTEIN (HUMAN)
 CC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 CC PRIMATES: CATARRHINI: HOMINIDAE: HOMO.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE-BONE MARROW;
 RC MEDLINE: 92396239.
 RA DELATRE O., ZUCKMAN J., PLOUGASTEL B., DESMAZE C., MELOT T.,
 RA "The human FLI-1 gene encodes a DNA-binding domain caused by chromosome
 RA translocation in human tumors.";
 RL NATURE 359:162-165(1992).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC MEDLINE: 93075640.
 RA WATSON D.R., SMITH P.E., THOMPSON D.M., CHENG J.O., TESTA J.R.,
 RA "The ETS-1 gene: isolation and characterization of a new member
 RT of the family of human ETS transcription factors.";
 RL CELL GROWTH DIFFER. 3:705-713(1992).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC MEDLINE: 93007976.
 RA PRASAD D.D., RAO V.N., REDDY E.S.;
 RT "Structure and expression of human flt-1 gene.";
 RL CANCER RES. 52:5833-5837(1992).
 RN [4]
 RN SEQUENCE FROM N.A.
 RC TISSUE-BLOOD;
 RC MEDLINE: 93176799.
 RA HROMAS R., MAY W., DENNY C., PARKIN W., MOORE J., MARI R.A.,
 RA BECK E., KLEMSZ M.J.;
 RT "Human flt-1 localizes to chromosome 11q24 and has an aberrant
 RT transcript in neuroepithelioma.";
 RL BLOOD. 81:1121-1125(1993).
 RN [5]
 RN STRUCTURE BY NMR OF 276-373.
 RA MEDLINE: 95297091.
 RA LIANG H., MAO X., OLEJNICZAK E.T., NETTESHEIM D.G., YU L.,
 RA MEADOWS R.P., THOMPSON C.B., FESIK S.W.;
 RT "Solution structure of the ets domain of flt-1 when bound to DNA.";
 RL NAT. STRUCT. BIOL. 1:871-875(1994).
 CC -1- FUNCTION: SEQUENCE SPECIFIC TRANSCRIPTIONAL ACTIVATOR. RECOGNIZES
 CC -1- THE DNA SEQUENCE 5' C[CA]GGAAGT-3'.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- TISSUE: BONE MARROW; BLOOD; LYMPH; THYMUS; SPLEEN; THYROID;
 CC CHROMOSOMAL TRANSLOCATION T(11;22)(Q24;Q12) WHICH INVOLVES FLI1

CC AND EMS.

1- SIMILARITY: BELONGS TO THE ETS FAMILY

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[illegible]

Query Match	15.1%;	Score 270;	DB 1;	length 452;
Best Local SImilarity	25.9%;	Prod No 9	20-14	

[illegible]

DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE ETS-RELATED PROTEIN TEL (ETS TRANSLLOCATION VARIANT 6)
GN ERV6 OR TEL.

OS	MUS MUSCULUS (MOUSE).
CC	EXARVOTIA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CC	ROENTIIA; SCIROGAMPHI; MURIDAE; MURINAE; MUS.
CC	(1)
CC	SEQUENCE FROM N.A.
CC	SWISS-PROT/1751/63/.
CC	BERNARD O
CC	1-1 SIMILARITY: BELONGS TO THE ETS FAMILY
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CC	EMBL; Y07915; E274398; .
CC	MSD; MGI:109336; EYVE
CC	PROSITE; PS00346; ETS_DOMAIN.1; FALSE-NEG.
CC	PROSITE; PS00346; ETS_DOMAIN.2; 1
CC	PROSITE; PS00661; ETS_DOMAIN.3; 1
CC	PFAM; PF00178; Ets; 1
CC	HSP; Q01543; IFLI
CC	NUCLEAR PROTEIN; DNA-BINDING.
CC	DNA_BIND 335 416 ETS-DOMAIN
CC	SEQUENCE 485 AA; 56405 MW; CAA5087 CRC32;

Query Match	14.9%	Score 265.5	DB 1	Length 485
Best Local Similarity	21.9%	Pred. No. 2e+13		
Matches	98	Conservative	47	Mismatches
			80	Indels
			223	Gaps
				15

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Db      2  SETPAOSSIKQERISYTPESP-----VASHRSTPLHVHTVPRALRMEEDSIH--

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[illegible]


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OY 233 -----ESWTDE-----VDSC----- 245
      |||
Db 289 FESTESLLHSMTSSSLVDMORVPSPSYDFEEDGNQTLINKQPMSPFNDYIDRCEPAELG 348
OY 245 -----SCOPILHNOFLKELLAPHSYGRFIRMLNKEKGIRFIEDSAOVARL 290
      |||
Db 349 KPIVASILAGFTGSG-PLOLHOFLE-LTDTKSCOSFISMTG-DOHEFYLDNDEVIARR 405
      |||
OY 291 WGIKRNBPANNDKLSRSIRQYKKGIIKRPDISORLYOFPV 332
      |||
Db 406 WCKRRNKPKMNEYKLSRGLRYYYDKNIHNTS-GKRYYYRFV 446
      |||
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Search completed: November 20, 1999, 15:17:38
Job time: 37 sec

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